II. AMENDMENTS TO THE SPECIFICATION

On page 1, please **replace** the paragraph beginning on line 23 and ending on page 2, line 4 with the following amended paragraph:

- - When the three dimensional structure of the target protein is known, it is possible to apply certain computational procedures which apply to the three dimensional steric and electrostatic constraints of the binding site as a basis, toward an electronic search of large and diverse chemical structure databases. Putative ligands are selected from the data and are scored on the basis of their "goodness of fit" to the binding site. Algorithms for this technique are widely known and used, and include MCSS/hook, dock leapfrog, and receptor. Although there are reports of success, the approach is limited in that true ligand/receptor flexibility is not accounted for, explicit water molecules are not included in the procedure and the energy functions used to calculate thermodynamic parameters and docking scores are overly simplified. Compounding these problems are the clock speeds of modern computers' microprocessors which are many orders of magnitude too slow. - -